SEQUENCE LISTING

<110>	IMMUNE Carter Zhou,	, Pa	ul J	•	ON										
<120>	ANTIBO	DIES	THA	т ві	נ ממ:	NTE	LEUF	CIN-4	REC	EPTC	R				
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acc to	gc gtc ys Val 35	tcc Ser	gac Asp	tac Tyr	atg Met	agc Ser 40	atc Ile	tct Ser	act Thr	tgc Cys	gag Glu 45	tgg Trp	aag Lys	atg Met	144
Asn G	gt ccc ly Pro 0	acc Thr	aat Asn	tgc Cys	agc Ser 55	acc Thr	gag Glu	ctc Leu	cgc Arg	ctg Leu 60	ttg Leu	tac Tyr	cag Gln	ctg Leu	192
gtt t Val P 65	tt ctg he Leu	ctc Leu	tcc Ser	gaa Glu 70	gcc Ala	cac His	acg Thr	tgt Cys	atc Ile 75	cct Pro	gag Glu	aac Asn	aac Asn	gga Gly 80	240
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gat a Asp A	ac tat sn Tyr	aca Thr 100	ctg Leu	gac Asp	ctg Leu	tgg Trp	gct Ala 105	GТĀ	cag Gln	cag Gln	ctg Leu	ctg Leu 110	tgg Trp	aag Lys	336

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												ctc Leu				480)
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cca Pro	agt Ser 450	gca Ala	Gly	ccc Pro	aag Lys	gag Glu 455	gca Ala	cct Pro	ccc Pro	tgg Trp	ggc Gly 460	aag Lys	gag Glu	cag Gln	cct Pro	1392
ctc Leu 465	cac His	ctg Leu	gag Glu	cca Pro	agt Ser 470	cct Pro	cct Pro	gcc Ala	agc Ser	ccg Pro 475	acc Thr	cag Gln	agt Ser	cca Pro	gac Asp 480	1440
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agc Ser 625	agt Ser	Gl ^à aaa	gaa Glu	gag Glu	630 ggg	tat Tyr	aag Lys	cct Pro	ttc Phe	caa Gln 635	gac Asp	ctc Leu	att Ile	cct Pro	ggc Gly 640	1920
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gtg Val	gga Gly	ccc Pro	aca Thr	Туг	atg Met	agg Arg	gto Val	tct Ser 825	:							2475

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Leu Leu Gln Val Ala Ser Ser Gly Asn Met Lys Val Leu Gln Glu Pro

Thr Cys Val Ser Asp Tyr Met Ser Ile Ser Thr Cys Glu Trp Lys Met

Asn Gly Pro Thr Asn Cys Ser Thr Glu Leu Arg Leu Leu Tyr Gln Leu

Val Phe Leu Leu Ser Glu Ala His Thr Cys Ile Pro Glu Asn Asn Gly

Gly Ala Gly Cys Val Cys His Leu Leu Met Asp Asp Val Val Ser Ala 85

Asp Asn Tyr Thr Leu Asp Leu Trp Ala Gly Gln Gln Leu Leu Trp Lys 105 100

Gly Ser Phe Lys Pro Ser Glu His Val Lys Pro Arg Ala Pro Gly Asn 120

Leu Thr Val His Thr Asn Val Ser Asp Thr Leu Leu Leu Thr Trp Ser 135

Asn Pro Tyr Pro Pro Asp Asn Tyr Leu Tyr Asn His Leu Thr Tyr Ala 155 150.

Val Asn Ile Trp Ser Glu Asn Asp Pro Ala Asp Phe Arg Ile Tyr Asn 170 165

Val Thr Tyr Leu Glu Pro Ser Leu Arg Ile Ala Ala Ser Thr Leu Lys 180 185

Ser Gly Ile Ser Tyr Arg Ala Arg Val Arg Ala Trp Ala Gln Cys Tyr 200

Asn Thr Thr Trp Ser Glu Trp Ser Pro Ser Thr Lys Trp His Asn Ser 215 220 210

Tyr Arg Glu Pro Phe Glu Gln His Leu Leu Gly Val Ser Val Ser Cys Ile Val Ile Leu Ala Val Cys Leu Leu Cys Tyr Val Ser Ile Thr Lys Ile Lys Lys Glu Trp Trp Asp Gln Ile Pro Asn Pro Ala Arg Ser Arg Leu Val Ala Ile Ile Ile Gln Asp Ala Gln Gly Ser Gln Trp Glu Lys Arg Ser Arg Gly Gln Glu Pro Ala Lys Cys Pro His Trp Lys Asn Cys Leu Thr Lys Leu Leu Pro Cys Phe Leu Glu His Asn Met Lys Arg Asp Glu Asp Pro His Lys Ala Ala Lys Glu Met Pro Phe Gln Gly Ser Gly Lys Ser Ala Trp Cys Pro Val Glu Ile Ser Lys Thr Val Leu Trp Pro Glu Ser Ile Ser Val Val Arg Cys Val Glu Leu Phe Glu Ala Pro Val Glu Cys Glu Glu Glu Glu Glu Glu Glu Glu Lys Gly Ser Phe Cys Ala Ser Pro Glu Ser Ser Arg Asp Phe Gln Glu Gly Arg Glu Gly Ile Val Ala Arg Leu Thr Glu Ser Leu Phe Leu Asp Leu Leu Gly Glu Glu Asn Gly Gly Phe Cys Gln Gln Asp Met Gly Glu Ser Cys Leu Leu Pro Pro Ser Gly Ser Thr Ser Ala His Met Pro Trp Asp Glu Phe Pro Ser Ala Gly Pro Lys Glu Ala Pro Pro Trp Gly Lys Glu Gln Pro

Leu His Leu Glu Pro Ser Pro Pro Ala Ser Pro Thr Gln Ser Pro Asp 470 475 Asn Leu Thr Cys Thr Glu Thr Pro Leu Val Ile Ala Gly Asn Pro Ala 485 490 Tyr Arg Ser Phe Ser Asn Ser Leu Ser Gln Ser Pro Cys Pro Arg Glu 505 Leu Gly Pro Asp Pro Leu Leu Ala Arg His Leu Glu Glu Val Glu Pro Glu Met Pro Cys Val Pro Gln Leu Ser Glu Pro Thr Thr Val Pro Gln Pro Glu Pro Glu Thr Trp Glu Gln Ile Leu Arg Arg Asn Val Leu Gln 550 His Gly Ala Ala Ala Pro Val Ser Ala Pro Thr Ser Gly Tyr Gln 570 Glu Phe Val His Ala Val Glu Gln Gly Gly Thr Gln Ala Ser Ala Val Val Gly Leu Gly Pro Pro Gly Glu Ala Gly Tyr Lys Ala Phe Ser Ser Leu Leu Ala Ser Ser Ala Val Ser Pro Glu Lys Cys Gly Phe Gly Ala 615 Ser Ser Gly Glu Gly Tyr Lys Pro Phe Gln Asp Leu Ile Pro Gly 630 635 Cys Pro Gly Asp Pro Ala Pro Val Pro Val Pro Leu Phe Thr Phe Gly 650 645 Leu Asp Arg Glu Pro Pro Arg Ser Pro Gln Ser Ser His Leu Pro Ser 660 665 Ser Ser Pro Glu His Leu Gly Leu Glu Pro Gly Glu Lys Val Glu Asp 675 680 Met Pro Lys Pro Pro Leu Pro Gln Glu Gln Ala Thr Asp Pro Leu Val 695 700 690

Asp Ser Leu Gly Ser Gly Ile Val Tyr Ser Ala Leu Thr Cys His Leu 705 710 715 Cys Gly His Leu Lys Gln Cys His Gly Gln Glu Asp Gly Gln Thr 725 730 Pro Val Met Ala Ser Pro Cys Cys Gly Cys Cys Gly Asp Arg Ser 740 745 Ser Pro Pro Thr Thr Pro Leu Arg Ala Pro Asp Pro Ser Pro Gly Gly 755 760 765 Val Pro Leu Glu Ala Ser Leu Cys Pro Ala Ser Leu Ala Pro Ser Gly 770 775 780 Ile Ser Glu Lys Ser Lys Ser Ser Ser Phe His Pro Ala Pro Gly 785 790 795 800 Asn Ala Gln Ser Ser Ser Gln Thr Pro Lys Ile Val Asn Phe Val Ser 805 810 Val Gly Pro Thr Tyr Met Arg Val Ser 820 <210> 3 327 <211> <212> DNA <213> Artificial <220> <223> Light chain variable sequence <220> <221> CDS <222> (1)..(327) <400> 3 48 gaa att gtg ttg acg cag tct cca ggc acc ctg tct ttg tct cca ggg Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly 96 gaa aga gcc acc ctc tcc tgc agg gcc agt cag agt gtt agc agc agc Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser 144 tac tta gcc tgg tac cag cag aaa cct ggc cag gct ccc agg ctc ctc Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu 192 atc ttt ggt gca tcc agc agg gcc act ggc atc cca gac agg ttc agt Ile Phe Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser 50 55

ggc agt ggg tct ggg aca gac ttc act ctc acc atc agg aga ctg gag Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu 65 70 75 80	240
cct gaa gat ttt gca gtg tat tac tgt cag cag tat ggt agc tca cct Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro 85 90 95	288
ccg tgg acg ttc ggc caa ggg acc aag gtg gaa atc aaa Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys 100 105	327
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Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu 35 40 45	
Ile Phe Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser 50 60	
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu 65 70 75 80	
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	Ala Ser Ser A		c atc cca gac agg y Ile Pro Asp Arg 60	
			c acc atc agc aga u Thr Ile Ser Arg 75	
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Gly Trp Thr I			g gag atc aaa 1 Glu Ile Lys	. 327
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_	Thr Leu Ser C 20	Cys Arg Ala Se 25	er Gln Ser Val Ser 30	
Tyr Leu Ala 1 35	Trp Tyr Gln G	Gln Lys Pro Gl 40	y Gln Ala Pro Arg 45	Leu Leu
Ile Tyr Gly A		Arg Ala Pro Gl	y Ile Pro Asp Arg	Phe Ser

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu 70 75 Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Asp His Ser Ala 90 Gly Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys 105 <210> 7 <211> 327 <212> DNA <213> Artificial <220> <223> Light chain variable sequence <220> <221> CDS <222> (1)..(327) <400> 7 48 gaa att gtg ttg acg cag tct cca ggc acc ctg tct ttg tct ccg ggg Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly gaa aga gcc acc ctc tcc tgc agg gcc agt cag act gtt aac agc gac 96 Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Thr Val Asn Ser Asp 25 tac tta gcc tgg tac cag cag aaa ccg ggc cag gct ccc agg ctc ctc 144 Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu 192 atc tat ggt gca tcc agc agg gcc act ggc atc cca gac agg ttc agt Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser 240 ggc agt ggg tet ggg aca gae tte act ete ace ate age aga etg gag Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu 70 288 cct gaa gat ttt gca gtc tat tac tgt cag cag tat ggt agg tca cct Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Arg Ser Pro 90 ccg tgg acg ttc ggc caa ggg acc aaa gtg gat atc aaa 327 Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Asp Ile Lys 100 105 <210> 8 <211> 109 <212> PRT <213> Artificial

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_	Thr Leu Ser 20	Cys Arg Ala 25	Ser Gln Thr Val	Asn Ser Asp 30
Tyr Leu Ala 35	Trp Tyr Gln	Gln Lys Pro 40	Gly Gln Ala Pro 45	Arg Leu Leu
Ile Tyr Gly .	Ala Ser Ser	Arg Ala Thr 55	Gly Ile Pro Asp 60	Arg Phe Ser
Gly Ser Gly 65	Ser Gly Thr 70	Asp Phe Thr	Leu Thr Ile Ser 75	Arg Leu Glu 80
Pro Glu Asp	Phe Ala Val 85	Tyr Tyr Cys	Gln Gln Tyr Gly 90	Arg Ser Pro 95
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atc tat ggt gca tct agc agg gcc tct ggc atc cca gac agg ttc agt Ile Tyr Gly Ala Ser Ser Arg Ala Ser Gly Ile Pro Asp Arg Phe Ser 50 55 60	192
ggc agt ggg ttt ggg aca gac ttc act ctc acc atc agc aga ctg gag Gly Ser Gly Phe Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu 65 70 75 80	240
cct gaa gat ttt gca ata tat tac tgt cag cag tat ggt agc tca cct Pro Glu Asp Phe Ala Ile Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro 85 90 95	288
ccg tgg acg ttc ggc caa ggg acc aag gtg gaa atc aaa Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys 100 105	327
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Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu 35 40 45	
Ile Tyr Gly Ala Ser Ser Arg Ala Ser Gly Ile Pro Asp Arg Phe Ser 50 55 60	
Gly Ser Gly Phe-Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu 65 70 75 80	-
Pro Glu Asp Phe Ala Ile Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro 85 90 95	
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tac tta gcc Tyr Leu Ala 35	tgg tac cag Trp Tyr Gln	cag aaa cct Gln Lys Pro 40	ggc cag gct co Gly Gln Ala Pi 45	ro Arg Leu L	tc 144 eu
atc tat ggt Ile Tyr Gly 50	aca tcc tac Thr Ser Tyr	agg gcc act Arg Ala Thr 55	ggc atc cca ga Gly Ile Pro As 60	ac agg ttc a sp Arg Phe S	gt 192 er
ggc agt ggg Gly Ser Gly 65	tct ggg aca Ser Gly Thr 70	gac ttc act Asp Phe Thr	ctc acc atc ac Leu Thr Ile Th 75	cc aga ctg g hr Arg Leu G 8	lu
			cag cag tat go Gln Gln Tyr G 90		
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Tyr Leu Ala 35	Trp Tyr Gln	Gln Lys Pro 40	Gly Gln Ala P		eu

Ile Tyr Gly Thr Ser Tyr Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Thr Arg Leu Glu 70 Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro 85 90 Pro Trp Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys 100 <210> 13 <211> 327 <212> DNA <213> Artificial <220> <223> Light chain variable sequence <220> <221> CDS <222> (1)..(327) <400> 13 48 gat att gtg ctg acg cag act cca gcc acc ctg tct ttg tct cca ggg Asp Ile Val Leu Thr Gln Thr Pro Ala Thr Leu Ser Leu Ser Pro Gly 10 96 gaa aga gcc acc ctc tcc tgc agg gcc agt cag agt gtt ggc agc agc Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Gly Ser Ser 144 tac tta gcc tgg tac cag cag aga cct ggc cag gct ccc agg ctc ctc Tyr Leu Ala Trp Tyr Gln Gln Arg Pro Gly Gln Ala Pro Arg Leu Leu 40 192 atc tat ggt gca tcc agc agg gcc act ggc atc ccg gac agg ttc agt Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser 55 240 ggc agt ggg tct ggg aca gac ttc act ctc acg atc agc aga ctg gag Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu 70 75 288 cct gaa gat ttt gca gtg tat tat tgt cag cag tat gga agt tca cct Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro 327 ccg tgg atg ttc ggc caa ggg acc aag gtg gag atc aaa Pro Trp Met Phe Gly Gln Gly Thr Lys Val Glu Ile Lys 105

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Ser Gly I1 50	t ggt e Gly		Gly G										192
ggc cga tt Gly Arg Ph 65		Ile S											240
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Glu Val Gland Ser Leu Ar Ala Met Phase Ser Gly II	Tg Leu 20 ne Trp	Ser (Val 7	Cys A Arg G Gly G	Ala G Gln A 40 Gly A	ly Ser 25 la Pro 0	Gly Gly Asn	Phe Lys Tyr	Thr Gly Ala 60	Phe Leu 45	Ser 30 Glu Ser	Arg Trp Val	Asn Val Lys	
Glu Val Gla Ser Leu Ar Ala Met Pl Ser Gly II 50 Gly Arg Pl	Tg Leu 20 ne Trp	Ser (Val 7)	Cys A Arg G Gly G 5 Ser A	Ala G Gln A 40 Gly A 55	ly Ser 25 la Pro 0 la Thr	Gly Gly Asn	Phe Lys Tyr Lys 75	Thr Gly Ala 60 Asn	Phe Leu 45 Asp	Ser 30 Glu Ser Leu	Arg Trp Val	Asn Val Lys Leu 80	

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Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn
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Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
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Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys
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                                                                      240
ggc cga ttc acc atc tcc aga gac aat gcc aag aac tcc ttg tat ctt
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
                                                                      288
caa atg aac agc ctg agt gcc gag gac atg gct gtg tat tac tgt gca
Gln Met Asn Ser Leu Ser Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala
                                                                      336
aga ggg agg tac tac ttc acc cac tgg ggc cag gga acc ctg gtc acc
Arg Gly Arg Tyr Tyr Phe Thr His Trp Gly Gln Gly Thr Leu Val Thr
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ggc cga Gly Arg 65	ttc ac	cc atc nr Ile	tcc Ser 70	aga Arg	gac Asp	aat Asn	gcc Ala	aag Lys 75	aac Asn	tcc Ser	ttg Leu	tat Tyr	ctt Leu 80	240
caa atg Gln Met	aac ag Asn Se	gc ctg er Leu 85	aga Arg	gcc Ala	gag Glu	gac Asp	atg Met 90	gct Ala	gtg Val	tat Tyr	tac Tyr	tgt Cys 95	gca Ala	288
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Ala Met	Phe T	rp Val	Arg	Gln	Ala 40	Pro	Gly	Lys	Gly	Leu 45	Glu	Trp	Val	
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Gly Arg 65	Phe T	hr Ile	Ser 70	Arg	Asp	Asn	Ala	Lys 75	Asn	Ser	Leu	Tyr	Leu 80	
Gln Met	Asn S	er Leu 85	Arg	Ala	Glu	Asp	Met 90	Ala	Val	Tyr	Tyr	Суs 95	Ala	
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Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn
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Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
caa atg aac agc ctg aga gcc gag gac atg gct gtg tat tac tgt gca
                                                                      288
Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala
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aga ggg agg tac tac ttc ccg tgg tgg ggc cag gga acc ctg gtc acc
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Ser	Gly 50	Ile	Gly	Thr	Gly	Gly 55	Ala	Thr	Asn	Tyr	Ala 60	Asp	Ser	Val	Lys		
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tco Sei	cto Lev	aga Arg	cto Leu 20	tco Ser	tgt Cys	gca Ala	ggc	tct Ser 25	: Gly	tto Phe	acc Thr	tto Phe	agt Ser 30	aga Arg	aat Asn	ğ	96
gct Ala	atg a Met	tto Phe 35	tgg Trp	gtt Val	cgc Arg	cag Gln	gct Ala 40	cca Pro	gga Gly	a aaa 7 Lys	ggt Gly	cto Lev 45	g gag ı Glu	tgg Trp	gta Val	14	14
tca Se:	a ggt c Gly 50	ati	ggt Gly	act Thi	ggt Gly	ggt Gly 55	gco Ala	c aca a Thr	a aad Asi	c tat n Tyr	gca Ala	a gad a Asp	c tco Ser	gtç Val	, aag Lys	19	92
gg: Gl: 65	c cga y Arg	a tto g Pho	c acc	ato r Ile	tcc Ser 70	aga Arg	gad Asj	c aat o Asr	gco n Ala	c aag a Lys 75	g aad s Asi	tco n Sei	c ttg r Lei	g tat ı Tyı	ctt Leu 80	24	40

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tcc Ser	ctg Leu	aga Arg	ctc Leu 20	tcc Ser	tgt Cys	gca Ala	ggc	tct Ser 25	gga Gly	ttc Phe	acc Thr	ttc Phe	agt Ser 30	aga Arg	aat Asn	96	;
gct Ala	atg Met	ttc Phe 35	tgg Trp	gtt Val	cgc Arg	cag Gln	gct Ala 40	cca Pro	gga Gly	aaa Lys	ggt Gly	ctg Leu 45	gag Glu	tgg Trp	gta Val	144	1
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aga Arg	G1A aaa	agg Arg	tac Tyr 100	${ t Trp}$	tac Tyr	ccg Pro	tgg Trp	tgg Trp 105	ggc Gly	cag Gln	gga Gly	acc Thr	ctg Leu 110	gtc Val	acc Thr	33	6
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Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val 40 Ser Gly Ile Gly Thr Gly Gly Ala Thr Asn Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala 90 Arg Gly Arg Tyr Trp Tyr Pro Trp Trp Gly Gln Gly Thr Leu Val Thr 105 Val Ser Ser 115 <210> 27 <211> 345 <212> DNA <213> Artificial <220> <223> Heavy chain variable sequence <220> <221> CDS <222> (1)..(345) <400> 27 48 gag gtt cag ctg gtg cag tct ggg gga ggc ttg gta cat cct ggg ggg Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val His Pro Gly Gly tcc ctg aga ctc tcc tgt gca ggc tct gga ttc acc ttc agt aga aat 96 Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn gct atg ttc tgg gtt cgc cag gct cca gga aaa ggt ctg gag tgg gta 144 Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val 192 tca ggt att ggt act ggt gcc aca agc tat gca gac tcc gtg aag Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys 55 240 ggc cga ttc acc atc tcc aga gac aat gcc aag aac tcc ttg tat ctt Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu 288 caa atg aac agc ctg aga gcc gag gac atg gct gtg tat tac tgt gca Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala 85 90

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aga Arg	GJÀ âââ	agg Arg	tac Tyr 100	tgg Trp	ttc Phe	ccg Pro	tgg Trp	tgg Trp 105	ggc	cag Gln	gga Gly	acc Thr	ctg Leu 110	gtc Val	acc Thr	336
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Ala	. Met	: Phe	. Trţ	Va]	L Arg	g Glr	Ala 40	Pro	G17	, Lys	Gly	/ Let 45	ı Glı	ı Tr <u>ı</u>	Val	

Ser Gly Ile Gly Thr Gly Gly Ala Thr Asn Tyr Ala Asp Ser Val Lys 50 Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu 75 Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala 85 Arg Gly Arg Tyr Trp Phe Pro Trp Trp Gly Gln Gly Thr Leu Val Thr 105 100 Val Ser Ser 115 <210> 31 <211> 345 <212> DNA <213> Artificial <220> <223> Heavy chain variable sequence <220> <221> CDS <222> (1)..(345) gag gtt cag ctg gtg cag tct ggg gga ggc ttg gta cat cct ggg ggg 48 Glu Val Gln Leu Val Gln Ser Gly Gly Leu Val His Pro Gly Gly 10 96 tec etg aga etc tec tgt gea gge tet gga tte ace tte agt aga aat Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn 25 144 gct atg ttc tgg gtt cgc cag gct cca gga aaa ggt ctg gag tgg gta Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val 192 tca ggt att ggt act ggt ggt gcc aca agc tat gca gac tcc gtg aag Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys 55 ggc cga ttc acc atc tcc aga gac aat gcc aag aac tcc ttg tat ctt 240 Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu caa atg aac agc ctg aga gcc gag gac atg gct gtg tat tac tgt gca 288 Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala 336 aga ggg agg tac tgg ttc ccg tgg tgg ggc cag gga acc ctg gtc acc Arg Gly Arg Tyr Trp Phe Pro Trp Trp Gly Gln Gly Thr Leu Val Thr 105 100

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caa atg aac agc c Gln Met Asn Ser I 8	ctg aga gcc gag Leu Arg Ala Glu 35	g gac atg gct 1 Asp Met Ala 90	Val Tyr Tyr (ogt gca 288 Cys Ala 95
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Ser Gly Ile Gly	Thr Gly Gly Al 55	a Thr Asn Tyr	Ala Asp Ser 60	Val Lys

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ggc cga ttc acc atc tcc aga gac aat gcc aag aac tcc ttg tat ctt Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu 65 70 75 80	240
caa atg aac agc ctg aga gcc gag gac atg gct gtg tat tac tgt gca Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala 85 90 95	288
aga ggg agg tac tac ttc ccg tgg tgg ggc cag gga acc ctg gtc acc Arg Gly Arg Tyr Tyr Phe Pro Trp Trp Gly Gln Gly Thr Leu Val Thr 100 105 110	336
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Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys 50 55 60	
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu 65 70 75 80	

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35

40

45

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Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys

50 55 60

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Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
65 70 75 80

caa atg aac agc ctg agt gcc gag gac atg gct gtg tat tac tgt gca 288
Gln Met Asn Ser Leu Ser Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala
85 90 95

aga ggg agg tac tac ttc ccg tgg tgg ggc cag gga acc ctg gtc acc

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gct atg ttc tgg gtt cgc cag gct cca gga aaa ggt ctg gag tgg gta Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val 35 40 45	144
tca ggt att ggt act ggt ggt gcc aca agc tat gca gac tcc gtg aag Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys 50 55 60	192
ggc cga ttc acc atc tcc aga gac aat gcc aag aac tcc ttg tat ctt Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu 65 70 75 80	240
caa atg aac agc ctg aga gcc gag gac acg gct gtg tat tac tgt gca Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr, Tyr Cys Ala 85 90 95	288
aga ggg agg tac tac ttc ccg tgg tgg ggc cag gga acc ctg gtc acc Arg Gly Arg Tyr Tyr Phe Pro Trp Trp Gly Gln Gly Thr Leu Val Thr 100 105 110	336
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- 10 15	
1 5 10 15 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Asn	·
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Asn 20 25 30 Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val	
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Asn 20 Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val 35 Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys	

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Ala	atg Met	ttc Phe 35	tgg Trp	gtt Val	cgc Arg	cag Gln	gct Ala 40	cca Pro	gga Gly	aaa Lys	ggt Gly	ctg Leu 45	gag Glu	tgg Trp	gta Val	144
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caa Gln	atg Met	aac Asn	agc Ser	ctg Leu 85	aga Arg	gcc Ala	gag Glu	gac Asp	acg Thr 90	gct Ala	gtg Val	tat Tyr	tac Tyr	tgt Cys 95	gca Ala	288
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<4°G1°1 Se	DOS. u Vai r Le a Me r G1 50	46 l Glr u Arg t Ph 35	n Let 20 e Trj	ı Val 5 ı Sei p Val	r Cys	ı Ser s Ala g Glı y Gl; 55	a Ala a Ala 40 y Al	a Ser 25 a Pro	10 r Gly o Gly r Se	y Pho y Ly: r Ty	e Thes Gl	r Phe y Let 45 a As	e Ser 30 u Gl	r Va	g Asn p Val	
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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Asn
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Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
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                                                                      192
Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys
                         55
ggc cga ttc acc atc tcc aga gac aat gcc aag aac tcc ttg tat ctt
                                                                      240
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
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Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
 aga ggg agg tac tgg tac aac aac tgg ggc cag gga acc ctg gtc acc
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Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys 50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu 65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala 85 90 95

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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Asn

20
25
30

gct atg ttc tgg gtt cgc cag gct cca gga aaa ggt ctg gag tgg gta

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35

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WO 2005/047331

Val Ser Ser

115

PCT/US2004/037242

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gct a Ala M	tg tt et Ph 35	ie Ti	rb /	gtt /al	cgc Arg	cag Gln	gct Ala 40	cca Pro	gga Gly	aaa Lys	ggt Gly	ctg Leu 45	gag Glu	tgg Trp	gta Val	144
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ggc c Gly A		tc a he T	cc a	atc Ile	tcc Ser 70	aga Arg	gac Asp	aat Asn	gcc Ala	aag Lys 75	aac Asn	tcc Ser	ttg Leu	tat Tyr	ctt Leu 80	240
caa a Gln N	atg a Met A	ac a sn S	er	ctg Leu 85	aga Arg	gcc	gag Glu	gac Asp	acg Thr 90	gct Ala	gtg Val	tat Tyr	tac Tyr	tgt Cys 95	gca Ala	288
aga (Arg (ggg a Gly A	rg 1	ac Yr 100	tgg Trp	tac Tyr	ccg Pro	tgg Trp	tgg Trp	, פדא	caç Glr	gga Gly	aco Thi	c cto Lev 110		acc Thr	336
gtc Val	tcc t Ser S	.ca Ser .15												•		345
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Ser Leu Arg	Leu Ser 20	Cys Ala	a Ala	Ser 25	Gly I	Phe T	hr. P	he S	er Al O	rg As	sn	
Ala Met Phe 35	Trp Val	Arg Gl	n Ala 40	Pro	Gly 1	Lys G	ly I	ieu G 15	lu T	rp V	al '	
Ser Gly Ile	Gly Thr	Gly Gl 55	y Ala	Thr	Ser	Tyr P	Ala <i>I</i> 50	Asp S	er V	al L	уs	
Gly Arg Phe 65	Thr Ile	Ser Ar 70	g Asp	Asn	Ala	Lys <i>1</i> 75	Asn :	Ser I	eu T	yr I 8	ieu 10	
Gln Met Asn	Ser Leu 85	ı Arg Al	a Glu	, Asp	Thr 90	Ala '	Val	Tyr :	fyr C	ys <i>F</i> 95	Ala	
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Val Ser Ser 115												
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tcc ctg ag Ser Leu Ar	a ctc to g Leu S 20	cc tgt er Cys	gca go Ala A	cc to la Se 25	ST. GT	a ttc y Phe	aco Thr	ttc Phe	agt Ser 30	aga Aŗg	aat Asn	96
gct atg tt Ala Met Ph 35	c tgg g ne Trp V	tt cgc al Arg	cag g Gln A 4	Ta Pi	ca gg co Gl	a aaa y Lys	a ggt s Gly	t ctg y Leu 45	gag Glu	tgg Trp	gta Val	144
tca ggt at Ser Gly II		ct ggt hr Gly	ggt g Gly A 55	cc a	ca aa hr As	c tat n Tyi	gca r Ala	a vor	tcc Ser	gtg Val	aag Lys	192

ggc Gly 65	cga Arg	ttc Phe	acc Thr	atc Ile	tcc Ser 70	aga Arg	gac Asp	aat Asn	gcc Ala	aag Lys 75	aac Asn	tcc Ser	ttg Leu	tat Tyr	ctt Leu 80	240
	atg Met	aac Asn	agc Ser	ctg Leu 85	aga Arg	gcc Ala	gag Glu	gac Asp	acg Thr 90	gct Ala	gtg Val	tat Tyr	tac Tyr	tgt Cys 95	gca Ala	288
aga Arg	ggg	agg Arg	tac Tyr 100	tgg Trp	tac Tyr	ccg Pro	tgg Trp	tgg Trp 105	ggc	cag Gln	gga Gly	acc Thr	ctg Leu 110	gtc Val	acc Thr	336
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Se	r Le	u Ar	g Le 20	u Se	r Cy:	s Ala	a Ala	a Se: 25	r Gl	y Ph	e Th	r Ph	e Se: 30	r Ar	g Asn	
Al	a Me	t Ph 35		p Va	l Ar	g Gl:	n Al 40	a Pr	o Gl	у Гу	rs Gl	у Le 45	u Gl	u Tr	p Val	
Se	r Gl 50		e Gl	y Th	r Gl	y Gl: 55	y Al	a Th	ır As	sn Ty	r Al 60	a As	p Se	r Va	l Lys	
G1 65		g Ph	ie Th	ır Il	.e Se 70	er Ar	g As	ap As	sn Al	la Ly 75	ys As S	sn S∈	er Le	u Ty	r Leu 80	L
G]	n Me	et As	sn Se	er Le 89		g Al	.a G]	lu As	sp Tl 9	hr Al	la Va	al Ty	r Ty	r C <u>)</u> 95	ys Ala S	a.
Aı	rg G	ly A:		yr T: 00	rp T)	yr Pi	o Ti	rp Ti	rp G 05	ly G	ln G	ly Tì	nr Le 13	eu Va LO	al Thi	r
V	al S	er S	er 15													
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aga ggg Arg Gly	agg tac Arg Tyr 100	Trp	ttc Phe	ccg Pro	tgg Trp	tgg Trp 105	ggc Gly	cag Gln	gga Gly	acc Thr	ctg Leu 110	gtc Val	acc Thr	336
gtc tcc Val Ser														345
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Ala Met	Phe Tr	o Val	Arg	Gln	Ala 40	Pro	Gly	Lys	Gly	Leu 45	Glu	Trp	Val	
Ser Gly 50	Ile Gl	y Thr	Gly	Gly 55	Ala	Thr	Asn	Tyr	Ala 60	Asp	Ser	Val	Lys	
Gly Arg 65	Phe Th	r Ile	Ser	Arg	Asp	Asn	Ala	Lys 75	Asn	Ser	Leu	Туr	Leu 80	
Gln Met	Asn Se	r Lev 85	ı Arg	Ala	Glu	. Asp	Thr 90	Ala	. Val	Tyr	Туг	Cys 95	Ala	
Arg Gly	Arg Ty) Phe	Pro	Trp	Trp 105		Gln	. Gly	Thr	Leu 110	Val	Thr	
Val Ser	Ser 115													
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tcc Ser	ctg Leu	aga Arg	ctc Leu 20	tcc Ser	tgt Cys	gca Ala	gcc Ala	tct Ser 25	gga Gly	ttc Phe	acc Thr	ttc Phe	agt Ser 30	aga Arg	aat Asn	96
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caa Gln	atg Met	aac Asn	agc Ser	ctg Leu 85	aga Arg	gcc Ala	gag Glu	gac Asp	acg Thr 90	gct Ala	gtg Val	tat Tyr	tac Tyr	tgt Cys 95	gca Ala	288
aga Arg	Gly ggg	agg Arg	tac Tyr 100	Trp	tac Tyr	ccg Pro	tgg Trp	tgg Trp 105	GTA	cag Gln	gga Gly	acc Thr	ctg Leu 110	val	acc Thr	336
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Sei	r Le	u Ar	g Let 20	ı Se:	r Cys	s Ala	a Ala	a Se: 25	r Gly	y Pho	e Th	r Phe	e Se: 30	r Ar	g Asn	

Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val 40 35 Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys 55 50 Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu 70 Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala 85 Arg Gly Arg Tyr Trp Tyr Pro Trp Trp Gly Gln Gly Thr Leu Val Thr 105 100 Val Ser Ser 115 <210> 61 <211> 345 <212> DNA <213> Artificial <220> <223> Heavy chain variable sequence <220> <221> CDS <222> (1)..(345) <400> 61 gag gtt cag ttg gtg gag tct ggg gga ggc ttg gta cag cct ggg ggg 48 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly 10 96 tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc agt aga aat Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Asn 144 gct atg ttc tgg gtt cgc cag gct cca gga aaa ggt ctg gag tgg gta Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val tca ggt att ggt act ggt ggt gcc aca aac tat gca gac tcc gtg aag 192 Ser Gly Ile Gly Thr Gly Gly Ala Thr Asn Tyr Ala Asp Ser Val Lys 50 240 ggc cga ttc acc atc tcc aga gac aat gcc aag aac tcc ttg tat ctt Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu 288 caa atg aac agc ctg aga gcc gag gac acg gct gtg tat tac tgt gca Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala 90 85

336 aga ggg agg tac tgg tac ccg tgg tgg ggc cag gga acc ctg gtc acc Arg Gly Arg Tyr Trp Tyr Pro Trp Trp Gly Gln Gly Thr Leu Val Thr 105 100 345 gtc tcc tca Val Ser Ser 115 <210> 62 <211> 115 <212> PRT <213> Artificial <220> <223> Synthetic Construct <400> 62 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly 10 5 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Asn 25 20 Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val 40 35 Ser Gly Ile Gly Thr Gly Gly Ala Thr Asn Tyr Ala Asp Ser Val Lys 55 50 Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu 75 70 65 Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala 85 90 Arg Gly Arg Tyr Trp Tyr Pro Trp Gly Gln Gly Thr Leu Val Thr 105 100 Val Ser Ser 115 <210> 63 <211> 109 <212> PRT <213> Artificial <220> 27A1 light chain variable region <223> <400> 63

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Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser 20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu 35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser 50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu 65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro 85 90 95

Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
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Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
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Ser Leu Arg Leu Ser Cys Ser Ala Ser Gly Phe Thr Phe Ser Arg Tyr 20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Arg Gly Leu Glu Trp Val 35 40 45

Ala Ile Ile Trp Phe Glu Gly Asn Asn Gln Tyr Tyr Ala Asp Ser Val 50 55 60

Lys Gly Arg Phe Thr Val Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr 65 70 75 80

Leu Glu Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

PCT/US2004/037242 WO 2005/047331

Ala Arg Gly Lys Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val 105 100 Thr Val Ser Ser 115 <210> 65 <211> 107 <212> PRT <213> Artificial <220> <223> 5A1 light chain variable region <400> 65 Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly 15 10 Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Tyr 25 20 Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile 35 Tyr His Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly 55 50 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro 80 75 70 65 Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ser Asn Trp Pro Leu 95 90 85 Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys 105 100 !<210> 66 123 <211> <212> PRT <213> Artificial <220> <223> 5A1 heavy chain variable region <400> 66 Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val His Pro Gly Gly

10

5

15

Ser Leu Arg Leu Thr Cys Ala Gly Ser Gly Phe Thr Phe Ser Asn Phe 20 25 30

Val Met His Trp Val Arg Gln Thr Pro Gly Gln Gly Leu Glu Trp Val
35 40 45

Ser Ala Ile Gly Thr Gly Gly Gly Thr Tyr Tyr Ala Asp Ser Val Lys 50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Ser Ser Leu Tyr Leu 65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala 85 90 95

Arg Asp Arg Pro Met Val Arg Gly Val Ile Ile Asp Tyr Phe Asp Tyr 100 105 110

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser 115 120

<210> 67

<211> 107

<212> PRT

<213> Artificial

<220>

<223> 63 light chain variable region

<400> 67

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val Gly 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Thr Trp 20 25 30

Leu Ala Trp Tyr Gln His Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile $35 \hspace{1.5cm} 40 \hspace{1.5cm} 45$

Tyr Val Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ala Asn Ser Phe Pro Phe 85 90 95

Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
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<220>

<223> 63 heavy chain variable region

<400> 68

Glu Val Gln Val Leu Glu Ser Gly Gly Asn Leu Val Gln Pro Gly Gly 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr 20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val 35 40 45

Ser Ser Ile Thr Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Ile Phe Tyr Cys
85 90 95

Ala Lys Asp Asn Arg Gly Phe Phe His Tyr Trp Gly Gln Gly Thr Leu 100 105 110

Val Thr Val Ser Ser 115

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Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Asn Arg 20 Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile 40 Tyr Ile Ala Ser Ile Led Gln Arg Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Thr Arg Leu Gln Pro 75 70 Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ala Asn Ser Phe Pro Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys 100 . 105 <210> 70 <211> 36 <212> DNA <213> Artificial <220> <223> Primers <220> <221> misc_featurė
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205

200

195

Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg 210 215 220

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys 225 230 235 240

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp 245 250 255

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys 260 265 270

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser 275 280 285

Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser 290 295 300

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser 305 310 315 320

Leu Ser Leu Ser Leu Gly Lys 325